SEQUENCE LISTING

<110> DIVERSA CORPORATION
SHORT, Jay

<120> WHOLE CELL ENGINEERING BY MUTAGENIZING A SUBSTANTIAL PORTION OF A STARTING GENOME, COMBINING MUTATIONS, AND OPTIONALLY REPEATING

<130> DIVER1510WO-1

<140> PCT/US 01/19367
<141> 2001-06-14

<150> US 09/677,584
<151> 2000-09-30

<150> US 09/594,459
<151> 2000-06-14

<160> 33

<170> PatentIn version 3.0

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<400> 2

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Phe Ser Ser Ala Ala Leu Gly Asp Pro Arg Arg Thr Ala Arg Leu Val
20 25 30

Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile
35 40 45

Ser Ser Glu Gly Ser Glu Ala Met Gln Glu Gly Ala Tyr Arg Phe Tyr
50 55 60

Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met
65 70 75 80

Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu
85 90 95

Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly
100 105 110

Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser
115 120 125

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Val Leu Leu Leu Glu Ala Thr Thr Phe Arg Thr Val Gly Leu Leu His
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Gln Glu Trp Trp Met Arg Pro Asp Asp Pro Ala Asp Ala Asp Glu Lys
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Glu Ser Gly Lys Trp Leu Ala Ala Ala Ala Thr Ser Arg Leu Arg Met
                165                 170                 175

Gly Ser Met Met Ser Asn Val Ile Ala Val Cys Asp Arg Glu Ala Asp
            180                 185                 190

Ile His Ala Tyr Leu Gln Asp Arg Leu Ala His Asn Glu Arg Phe Val
        195                 200                 205

Val Arg Ser Lys His Pro Arg Lys Asp Val Glu Ser Gly Leu Tyr Leu
    210                 215                 220

Ile Asp His Leu Lys Asn Gln Pro Glu Leu Gly Gly Tyr Gln Ile Ser
225                 230                 235                 240

Ile Pro Gln Lys Gly Val Val Asp Lys Arg Gly Lys Arg Lys Asn Arg
                245                 250                 255

Pro Ala Arg Lys Ala Ser Leu Ser Leu Arg Ser Gly Arg Ile Thr Leu
            260                 265                 270

Lys Gln Gly Asn Ile Thr Leu Asn Ala Val Leu Ala Glu Glu Ile Asn
        275                 280                 285

Pro Pro Lys Gly Glu Thr Pro Leu Lys Trp Leu Leu Leu Thr Gly Glu
    290                 295                 300

Pro Val Glu Ser Leu Ala Gln Ala Leu Arg Val Ile Asp Ile Tyr Thr
305                 310                 315                 320

His Arg Trp Arg Ile Glu Glu Phe His Lys Ala Trp Lys Thr Gly Ala
                325                 330                 335

Gly Ala Glu Arg Gln Arg Met Glu Glu Pro Asp Asn Leu Glu Arg Met
            340                 345                 350

Val Ser Ile Leu Ser Phe Val Ala Val Arg Leu Leu Gln Leu Arg Glu
        355                 360                 365

Ser Phe Thr Leu Pro Gln Ala Leu Arg Ala Gln Gly Leu Leu Lys Glu
    370                 375                 380

Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp
385                 390                 395                 400

Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys
                405                 410                 415

Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu
            420                 425                 430

Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala
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Leu Trp Glu Gly Trp Glu Ala Leu Gln Ser Lys Leu Asp Gly Phe Leu
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<223> n is A, T, G, or C

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<220>
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<212> PRT
<213> Artificial sequence

<220>
<223> Antibody spacer peptide. The entire peptide sequence can be repeated more than one time

<400> 5

Gly Gly Gly Gly Ser
1 5

<210> 6
<211> 14
<212> DNA
<213> Artificial sequence

<220>
<223> Tetradecanucleotide d

<400> 6
catgccatgg catg 14

<210> 7
<211> 21
<212> DNA
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<220>
<223> 21-mer d

<400> 7
aaattgtgca catcctgcag c 21

<210> 8
<211> 12
<212> DNA
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<220>
<223> 12-mer target DNA

<400> 8
agcctagctg aa 12

<210> 9
<211> 12
<212> DNA
<213> Artificial sequence

<220>
<223> Complement of the original 12-mer target

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tcggatcgac tt 12

<210> 10
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<220>
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<222> (3)..(3)
<223> Xaa is any Amino Acid

<400> 10

Tyr Tyr Xaa Tyr
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<210> 11
<211> 4
<212> PRT
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<220>
<223> Single base mismatched probe

<400> 11

Tyr Tyr Tyr Tyr
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<210> 12
<211> 4
<212> PRT
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<220>
<223> 4-mer extemtion probe

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is any Amino Acid

<400> 12

Tyr Xaa Tyr Tyr
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<210> 13
<211> 10
<212> DNA
<213> Artificial sequence

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<223> BstNB I cleaves btw. nucleotide 9 & 10 of target sequence

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<222> (6)..(10)
<223> n is any nucleotide

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gagtcnnnnn 10

<210> 14
<211> 223
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (1)..(10)
<223> at least one nt. of nt. 1-10 is present

<220>
<221> misc_feature
<222> (21)..(120)
<223> at least one nt. of nt. 21-120 is present

<220>
<221> misc_feature
<222> (124)..(223)
<223> nt. 124-223 are optionally present

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120

atgnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnn 223

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<211> 215
<212> DNA
<213> Artificial sequence

<220>
<223> Revers primer

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<222> (1)..(215)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (1)..(10)
<223> at least one nt. of nt. 1-10 is present

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<221> misc_feature
<222> (16)..(115)
<223> at least one nt. of 16-115 is present

<220>
<221> misc_feature
<222> (116)..(215)
<223> nt. 116-215 are optionally present

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnn 215

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<212> DNA
<213> Artificial sequence

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<223> Forward primer with 10-100 template specific sequence

<220>
<221> misc_feature

<222> (24)..(123)
<223> n is any nucleotide

<220>
<221> misc_feature
<222> (34)..(123)
<223> nt. 34-123 are each optionally present

<400> 16
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120

nnn 123

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<223> Reverse primer with 10-100 nt long template specific sequence

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<222> (32)..(121)
<223> nt. 32-121 are each optionally present

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120

n 121

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<400> 18
ctagaaggga ggagaaaacc atg 23

<210> 19
<211> 21
<212> DNA
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<220>
<223> Reverse primer

<400> 19

gatcaaaggc gcgcctgcag g 21

<210> 20
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aatgcctttt gtgacggacg tcgcccgatg 150

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<223> Protogenitor template 12412

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attccccacg ttgccggctt gggacgctg 149

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<223> Protogenitor template 124-1d

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catgccgcac ttggaagggc tgggccggct 150

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<223> Protogenitor template b3

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<223> Consensus sequence

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<211> 100
<212> DNA
<213> Artificial sequence

<220>
<223> Derived nucleic acid building block sequence

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gcttcgttcg acagtacaat cgatcaatta atggttcgag 100

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<212> DNA
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<223> Polynucleotide progenitor template 150am13_00

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gatgatcgtc ggcatgaaga ccggcctgcc cggaatggat ctggtgatct tcccggaata 180

ttcgacccac ggcatcatgt acgactccaa ggaaatgtac gataccgcgt ccgtcgtgcc 240

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gatcgaaggc tggtatcccg gcaactgcac gtacgtctcc gaaggcccga agggcatgaa 480

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cccgtatgat ttctattcga aatggatcgc cgatcccgag ggtacacgcg agatggtgga 960

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<212> DNA
<213> Artificial sequence

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catggtcgtg ggcatgaagc gcggcctgcc cggcatggac ctggtcatct tccccgagta 180

ctccacccac ggcatcatgt acgacgccaa ggaaatgtac gaaaccgctt cggccattcc 240

gggcgaagag actgctgtgt tcgccgacgc ctgccgcaag gccaacgtat ggggcgtgtt 300

ttcgctgacg ggcgagcgcc acgaagagca cccgaacaag gcgccgtaca acacgctcat 360

cctgatgaac aacaagggcg agatcgtgca gaagtaccgc aagatcatgc cctgggtgcc 420

gatcgaaggc tggtatccgg gcgattgcac ctatgtgtcg gaaggcccca agggactgaa 480

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